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Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2007; month=11; day=29; hr=12; min=6; sec=8; ms=469;]
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Reviewer Comments:
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<211> 33
<212> DNA
<213> Artificial

<220>
<223> Synthetic Construct

<220>
<221> misc_feature
<222> (22)..(24)
<223> The residues in these positions could be any amino acid

<400> 18
agggccagtc agttcgttgg cnnnagcatc cac 33

The above <223> response explaining the "n's" at locations 22-24 is incorrect. This is not an amino acid sequence; it is a nucleotide sequence. Same error in Sequences 24, 30, 32, 42, 48, and 52 (and possibly in subsequent sequences).
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Validated By CRFValidator v 1.0.3

Application No: 10541260 Version No: 2.0

Input Set:

Output Set:

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Finished: 2007-11-09 11:44:35.401
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 90 ms
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Total Errors: 0
No. of SeqIDs Defined: 122
Actual SeqID Count: 122

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Input Set:

Output Set:

Started: 2007-11-09 11:44:33.311
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Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 90 ms
Total Warnings: 104
Total Errors: 0
No. of SeqIDs Defined: 122
Actual SeqID Count: 122

Error code	Error Description

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<110> Watkins, Jeffry D.
Vasserot, Alain P.
Marquis , David
Huse , William D.

<120> TNF-alpha Binding Molecules

<130> X-16758M

<140> 10541260
<141> 2005-06-30

<150> PCT/US04/00290
<151> 2004-01-08

<150> 10/338,552
<151> 2003-01-08

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<160> 122

<170> PatentIn version 3.3

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1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Trp His Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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gatcagtctc caaagctcct catcaagtat gcttctgagt ctatgtctgg ggtcccctcg 180

aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct 240

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gggaccaagg tggaaatcaa a 321

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<212> PRT
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<223> Synthetic Construct

<400> 3

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser

65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

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ccagggaagg ggctggagtg ggttggcgaa attagatcaa aatctattaa ttctgcaaca 180

cattatgcgg agtctgtgaa agggagattc accatctcaa gagatgattc aaagaactca 240

ctgtacctgc agatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtgctaga 300

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<400> 5

Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Val Gly Tyr Ser
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

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Lys Tyr Ala Ser Glu Ser Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65                  70                  75                  80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Trp His Phe
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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gatcagtctc caaagctcct catcaagtat gcttctgagt ctaggtctgg ggtcccctcg    180

aggttcagtg gcagtggatc tgggacagat ttcaccctca ccatcaatag cctggaagct    240

gaagatgctg ccacgtatta ctgtcaacaa agtcatagct ggcatttcac gttcggccaa    300

gggaccaagg tggaaatcaa a                                              321
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<220>
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Ser Asn His
            20                  25                  30
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Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Gly Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr His Tyr Ala Glu
    50                  55                  60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65                  70                  75                  80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp His Trp Gly Gln
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Gly Thr Leu Val Thr Val Ser Ser
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<400> 8

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ccagggaagg ggctggagtg ggttggcgaa attagatcaa aatctatgaa ttctgcaaca    180

cattatgcgg agtctgtgaa agggagattc accatctcaa gagatgattc aaagaactca    240

ctgtacctgc agatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtgctaga    300

aattactacg gtagtaccta cgaccattgg ggccaaggga ccctggtcac cgtctcctca    360
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Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His
1 5 10

<210> 10
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<220>
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<400> 10
agggccagtc agttcgttgg ctcaagcatc cac 33

<210> 11
<211> 11
<212> PRT
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<400> 11

Arg Ala Ser Gln Phe Val Gly Leu Ser Ile His
1 5 10

<210> 12
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Arg Ala Ser Gln Phe Val Gly Met Ser Ile His
1 5 10

<210> 14

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<400> 15

Arg Ala Ser Gln Phe Val Gly Tyr Ser Ile His
1 5 10

<210> 16
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<400> 16
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<400> 17

Arg Ala Ser Gln Phe Val Gly Xaa Ser Ile His
1 5 10

<210> 18
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<400> 19

Tyr Ala Ser Glu Ser Met Ser
1 5

<210> 20
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<400> 20
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<210> 21
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<400> 21

Tyr Ala Ser Glu Tyr Met Ser
1 5

<210> 22
<211> 21
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<400> 22
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<210> 23
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1 5

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<220>

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<400> 25

Tyr Ala Ser Glu Ser Arg Ser
1 5

<210> 26
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<400> 26
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<210> 27
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<400> 27

Tyr Ala Ser Glu Ser Lys Ser
1 5

<210> 28
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<400> 28
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<400> 31

Tyr Ala Ser Glu Xaa Xaa Ser
1 5

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<210> 33
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<400> 33

Gln Gln Ser His Ser Trp His Phe Thr
1 5

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<210> 35
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<400> 35

Gly Phe Thr Phe Ser Asn His Trp Met Asn
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<400> 37

Gly Phe Lys Phe Ser Asn His Trp Met Asn
1 5 10

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Gly Phe Pro Phe Ser Asn His Trp Met Asn
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Val Lys Gly

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1 5 10 15

Val Lys Gly

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Val Lys Gly

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Val Lys Gly

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Val Lys Gly

<210> 52
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<400> 53

Asn Tyr Tyr Gly Ser Thr Tyr Asp His
1 5

<210> 54
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<400> 54
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<210> 55
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<400> 55

Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr His Tyr Ala Arg Ser
1 5 10 15

Val Lys Gly

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